
Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue May 15 12:31:12 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10571667 Version No: 1.1

Input Set:

Output Set:

Started: 2007-05-15 12:30:57.314 **Finished:** 2007-05-15 12:30:58.489

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 175 ms

Total Warnings: 10
Total Errors: 0

No. of SeqIDs Defined: 20

Actual SeqID Count: 20

Erro	or code	Error Description											
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(11)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(12)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(13)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(14)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(15)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(16)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(17)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(18)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(19)			
W	213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(20)			

```
<110> DE VRIES, Erik
GAFFAR, Fasilla Razzia
YATSUDA, Ana Patricia
SCHAAP, Theodorus Cornelis
<120> Piroplasmid vaccine
<130> I-2003.010 US
<140> 10/571,667
<141> 2006-03-14
<150> PCT/EP2004/052169
<151> 2004-09-14
<150> EP 03020898.7
<151> 2003-09-14
<160> 20
<170> PatentIn version 3.3
<210> 1
<211> 1818
<212> DNA
<213> Babesia bovis
<220>
<221> CDS
<222> (1)..(1818)
<400> 1
atg cag tta cat aac aaa atg cag tca act tct ctc aaa tat aac tac
                                                                      48
Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr
                5
                                    10
aag cgc atg ctt tgt atg gct ctt gta cca gtt atc tta tcg tca ttt
Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe
            20
                                25
ttt geg gaa gat get tta get tee aac tee aeg ett tte get tte eae
                                                                     144
Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His
        35
                            40
                                                45
aag gaa cca aac aat cgt agg ctt acc aaa agg tct tca aga gga cag
                                                                     192
Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
    50
ttg ctc aac tca agg agg ggt tcg gat gat gcg tcc gaa tct tcc gat
                                                                     240
Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
                    70
                                        75
```

aga tac cca ggt agg tcg ggt ggc tct aag aat tcg agc caa tcc ccc

288

Arg	Tyr	Pro	Gly	Arg 85	Ser	Gly	Gly	Ser	Lys 90	Asn	Ser	Ser	Gln	Ser 95	Pro	
		_		_	caa Gln	_		-			_					336
			-	-	ctt Leu				-		-				_	384
	_	_		_	ggt Gly	_	_		_	_					_	432
				_	gac Asp 150			_					-	-		480
_		_		_	gca Ala					-		_				528
				_	aca Thr	-					-			-		576
			-	_	gcg Ala		-	_	_	_				_		624
	_	_			tgc Cys		_		_	_					-	672
	_		_		aaa Lys 230						_		_	_	_	720
	_	_	_		ata Ile	_			_							768
			_	_	aac Asn	-		_		_	-			_		816
_		_	_		cct Pro		_		_		_	_				864
					gtt Val	-		_		- T	- T		_		-	912
		_		_	gcc Ala										_	960

305	310	315	320

gtt	gcc	att	gct	cct	gca	ttc	caa	gaa	tat	gcc	aac	agc	act	gaa	gac	1008
Val	Ala	Ile	Ala	Pro 325	Ala	Phe	Gln	Glu	Tyr 330	Ala	Asn	Ser	Thr	Glu 335	Asp	
_	_	_				_			_		gac Asp	_			_	1056
-	-		-	-			-			-	ttg Leu		-			1104
	_	_		_	_	_	_	_		_	att Ile 380					1152
		-	-			_	-			_	ggt Gly			_		1200
	-			_		_			_	_	gct Ala				_	1248
			_	_		_				_	att Ile	-		_	_	1296
							_	_	_		tat Tyr		_			1344
_					_	, ,		_	_	_	aat Asn 460					1392
	-	-				_			_	_	agc Ser	_	_			1440
	_	-	-		-			_			gac Asp	_	_			1488
			_		-	_					ttc Phe					1536
	_							_	_		gta Val				_	1584
_				-		_					ata Ile 540			_		1632

I		_	gct Ala				_	_			_		_				1680
	-		tat Tyr	-		-				-	-	_		-	_	_	1728
	_	_	ttg Leu	-			_		_				_	_		_	1776
		-	gat Asp 595	-			-							taa			1818
<	:210 :211 :212 :213	.> (?> I	2 605 PRT Babes	sia k	povis	3											
<	400)> 2	2														
M 1		Gln	Leu	His	Asn 5	Lys	Met	Gln	Ser	Thr 10	Ser	Leu	Lys	Tyr	Asn 15	Tyr	
I	īÀs	Arg	Met	Leu 20	Cys	Met	Ala	Leu	Val 25	Pro	Val	Ile	Leu	Ser 30	Ser	Phe	
Ρ	he	Ala	Glu 35	Asp	Ala	Leu	Ala	Ser 40	Asn	Ser	Thr	Leu	Phe 45	Ala	Phe	His	
I	ıys	Glu 50	Pro	Asn	Asn	Arg	Arg 55	Leu	Thr	Lys	Arg	Ser 60	Ser	Arg	Gly	Gln	
	ieu 55	Leu	Asn	Ser	Arg	Arg 70	Gly	Ser	Asp	Asp	Ala 75	Ser	Glu	Ser	Ser	Asp 80	
Α	rg	Tyr	Pro	Gly	Arg 85	Ser	Gly	Gly	Ser	Lys 90	Asn	Ser	Ser	Gln	Ser 95	Pro	
Т	rp	Ile	Lys	Tyr 100	Met	Gln	Lys	Phe	Asp 105	Ile	Pro	Arg	Asn	His 110	Gly	Ser	
G	Sly	Ile	Tyr	Val	Asp	Leu	Gly	Gly	Tyr	Glu	Ser	Val	Gly	Ser	Lys	Ser	

Tyr	Arg 130	Met	Pro	Val	Gly	Lys 135	Cys	Pro	Val	Val	Gly 140	Lys	Ile	Ile	Asp
Leu 145	Gly	Asn	Gly	Ala	Asp 150	Phe	Leu	Asp	Pro	Ile 155	Ser	Ser	Asp	Asp	Pro 160
Ser	Tyr	Arg	Gly	Leu 165	Ala	Phe	Pro	Glu	Thr 170	Ala	Val	Asp	Ser	Asn 175	Ile
Pro	Thr	Gln	Pro 180	Lys	Thr	Arg	Gly	Ser 185	Ser	Ser	Ala	Ser	Ala 190	Ala	Lys
		195				_	200					205	Tyr		_
	210					215					220		Ile		
225					230	_		_		235			Asp Asn		240
				245					250				Thr	255	
			260					265					270 His		
		275					280					285	Cys		
_	290			_		295					300		Gly		
305 Val	Ala	Ile	Ala	Pro	310 Ala	Phe	Gln	Glu	Tyr	315 Ala	Asn	Ser	Thr	Glu	320 Asp
				325					330				Asn	335	
4			340			•		345			•		350		

Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu

355 360 365

Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu 370 375 380 Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn 390 395 Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu 405 410 415 Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala 420 425 Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile 435 440 445 Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr 450 455 460 Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu 470 475 480 Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr 485 490 495 Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu 505 500 510 His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys 515 520 525 Cys Thr Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe 535 530 540 Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu 545 550 555 560 Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu 570 565

Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg

585

590

580

Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn 595 600 605

<213 <213	<210> 3 <211> 2349 <212> DNA <213> Theileria annulata															
<220 <220 <220	L> (CDS (1).	. (234	19)												
< 400)> :	3														
atg	aaa	aaa	ata	gga	ctt	aaa	att	agg	gca	caa	aag	gat	aaa	tta	aat	48
Met 1	Lys	Lys	Ile	Gly 5	Leu	Lys	Ile	Arg	Ala 10	Gln	Lys	Asp	Lys	Leu 15	Asn	
cct	ata	tta	gga	aσc	aac	tct	gac	cct	tca	σaa	αaα	tat	gat	tca	ttc	96
				-		Ser	-		_	-			-			
cad	caa	aat	att	ttc	act	cat	caa	cca	acc	caa	cta	cac	222	t ct	cat	144
_			_			His										144
cac	tac	att	aca	cac	cag	aaa	aaa	acc	agc	caa	cac	atc	gac	gat	tta	192
His	Tyr 50	Ile	Thr	His	Gln	Lys 55	Lys	Thr	Ser	Gln	His 60	Ile	Asp	Asp	Leu	
aat	ttt	tat	aat	gga	aaa	ttt	aat	caa	aag	agc	aga	att	ggt	cca	ggg	240
Asn	Phe	Tyr	Asn	Gly	Lys	Phe	Asn	Gln	Lys	Ser	Arg	Ile	Gly	Pro	Gly	
65					70					75					80	
_	-	-			-	agg -		_	_	_		_				288
Lys	Val	Val	Asn	Asn 85	ser	Arg	Asn	Leu	90	GIu	GIY	Glu	Thr	Leu 95	Ser	
aag	gat	gac	aat	aaa	aca	aaa	tct	aaa	ata	aag	tca	aaa	aca	gca	tca	336
Lys	Asp	Asp	Asn 100	Lys	Thr	Lys	Ser	Lys 105	Ile	Lys	Ser	Lys	Thr 110	Ala	Ser	
att	tta	cct	aga	ctt	tta	aaa	tct	tta	tca	ttt	tta	gct	gtt	tta	ggg	384
Ile	Leu	Pro	Arg	Leu	Leu	Lys	Ser	Leu	Ser	Phe	Leu	Ala	Val	Leu	Gly	
		115					120					125				
						tta	-			_						432
Ser	11e 130	Asn	Ser	Phe	Ser	Leu 135	Ala	Leu	Glu	Glu	Pro 140	Phe	Thr	Gln	His	
act	tct	aac	cga	acg	ccc	ttt	gaa	gta	tca	tta	att	caa	agc	aac	agc	480
Thr	Ser	Asn	Arg	Thr	Pro	Phe	Glu	Val	Ser	Leu	Ile	Gln	Ser	Asn	Ser	
145					150					155					160	

agt	tta	tcg	cct	att	cat	aat	tct	tca	act	caa	aat	tca	agt	cat	cac	528
Ser	Leu	Ser	Pro	Ile	His	Asn	Ser	Ser	Thr	Gln	Asn	Ser	Ser	His	His	
				165					170					175		
aac	ggt	ttt	agt	ggt	agt	acc	gtt	aat	aat	acc	tca	tta	ata	gag	aca	576
Asn	Gly	Phe	Ser	Gly	Ser	Thr	Val	Asn	Asn	Thr	Ser	Leu	Ile	Glu	Thr	
			180					185					190			
agg	aat	aac	gta	tta	aac	aga	aca	cta	ggt	aga	ttc	gga	tca	ttt	ttg	624
Arg	Asn	Asn	Val	Leu	Asn	Arg	Thr	Leu	Gly	Arg	Phe	Gly	Ser	Phe	Leu	
		195					200					205				
caa	tca	gga	ttg	ata	agc	agt	aga	gca	gac	aaa	aag	aag	cgg	tct	ggt	672
Gln	Ser	Gly	Leu	Ile	Ser	Ser	Arg	Ala	Asp	Lys	Lys	Lys	Arg	Ser	Gly	
	210					215					220					
atg	aat	aga	aga	ggc	cct	aag	ggg	aag	aaa	ggg	aag	gga	gga	gaa	gac	720
Met	Asn	Arg	Arg	Gly	Pro	Lys	Gly	Lys	Lys	Gly	Lys	Gly	Gly	Glu	Asp	
225					230					235					240	
gaa	gaa	aaσ	agg	aac	aaσ	taa	acc	gat	ttc	atσ	gca	aaσ	ttt	gat	atc	768
_	Glu	_				- 55		5		9	5	9		5		
	- L u	-70	9													